

GenCore version 5.1.7  
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 OM protein - protein search, using sw model  
 Run on: May 5, 2006, 13:58:01 ; Search time 46 Seconds  
 (without alignments)  
 564.351 Million cell updates/sec  
 Title: US-10-666-851-2  
 Perfect score: 1706  
 Sequence: 1 MGIGRSIGGRGALGVIA.....KINPMKCKMKNNHECPTFQSVFK 314  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched:

572060 seqB, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database : Issued Patents AA:  
 1: /cgn2\_6/ptodata/1/iaa/5\_COMB.dep: \*  
 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.dep: \*  
 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.dep: \*  
 4: /cgn2\_6/ptodata/1/iaa/PCBS\_COMB.dep: \*  
 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.dep: \*  
 6: /cgn2\_6/ptodata/1/iaa/bactfilesel.dep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1701	99.7	314	2	US-08-937-067-7
2	1691.5	99.5	313	2	US-08-937-067-7
3	1691.5	99.2	313	2	US-09-514-885-1
4	1657.5	97.2	313	2	US-09-949-016-6299
5	1657.5	97.2	313	2	US-09-946-043-3
6	1629	95.5	314	2	US-09-087-031B-3
7	1614.5	94.6	313	2	US-09-087-031B-4
8	1267.5	94.3	2	US-09-546-043-7	
9	1171	68.6	246	2	US-09-566-042-6
10	971	56.9	229	2	US-09-546-042-8
11	924.5	54.2	317	2	US-08-937-067-6
12	924.5	54.2	317	2	US-09-949-016-6300
13	911.5	53.4	305	2	US-09-949-016-7706
14	886.5	52.0	2	US-09-546-043-5	
15	605.5	35.5	295	2	US-08-937-067-2
16	598	35.1	295	2	US-09-939-832A-415
17	598	35.0	295	2	US-10-020-442A-415
18	597	35.0	295	2	US-09-148-545-179
19	597	35.0	295	2	US-09-621-011-179
20	597	35.0	2	US-09-148-541-237	
21	597	35.0	296	2	US-09-621-011-237
22	594	34.9	295	2	US-09-087-031B-19
23	508.5	29.8	295	2	US-08-893-652B-6
24	436	25.6	212	2	US-08-937-067-4
25	408.5	24.0	280	2	US-08-893-654B-4
26	227	28.7	281	2	US-08-893-652B-2
27	353	20.7	113	2	US-09-087-031B-24

## ALIGNMENTS

RESULT 1  
 US-08-937-067-7  
 Sequence 7, Application US/08937067  
 Patent No. 6433155  
 GENERAL INFORMATION:  
 APPLICANT: Umarbky, Samuil  
 ADDRESS: MORRISON & FOERSTER  
 STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304-0118  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/937,067  
 FILING DATE: CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lehnhardt, Susan K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 23647-20018:00  
 TELCOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 813-5600  
 TELEFAX: (650) 424-0792  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 314 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 Query Match Best Local Similarity 99.7%; Pred. No. 3.5e-174;  
 Matches 313; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QV 1 MGIGRSIGGRGALGVIA.....KINPMKCKMKNNHECPTFQSVFK 60  
 DB 1 MGIGRSIGGRGALGVIA.....KINPMKCKMKNNHECPTFQSVFK 60

RESULT 2  
US-09-514-885-1  
; Sequence 1, Application US/09514885  
; Patent No. 6656461  
; GENERAL INFORMATION:  
; APPLICANT: D'Armento, Jeanine  
; APPLICANT: Imai, Kazuhi  
; TITLE OF INVENTION: NOVEL THERAPEUTIC TREATMENT OF CHRONIC OBSTRUCTIVE  
FILE REFERENCE: 56483.app  
CURRENT APPLICATION NUMBER: US/09/514,885  
CURRENT FILING DATE: 2000-02-29  
NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 313  
TYPE: PRT  
; ORGANISM: Human  
US-09-514-885-1

Query Match 99.2%; Score 1691.5; DB 2; Length 313;  
Best Local Similarity 99.7%; Pred. No. 3.6e-13; Matches 313; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
Matches 313; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query 1 MGIGRSRRGGRRGAGLVLGALLGAGLAVGASASBYDVSFQSDIGPVQSGRPFYKPPQCV 60  
DB 1 MGIGRSRRGGRRG-ALGVLAAGLAVGASASBYDVSFQSDIGPVQSGRPFYKPPQCV 59

Query 61 IPADRURCHNRYKQWNLPLNLEHETWAKVOQASSWPLANKNCHAGTQVFLCSLFP 120  
DB 60 IPADRURCHNRYKQWNLPLNLEHETWAKVOQASSWPLANKNCHAGTQVFLCSLFP 119

Query 121 CDRPRTYPCRMCEAVRDSCFVSPMFGFVPEMLKCDKPPRGDVCTAMTPNATRASKP 180  
DB 120 CDRPRTYPCRMCEAVRDSCFVSPMFGFVPEMLKCDKPPRGDVCTAMTPNATRASKP 179

Query 61 MGIGRSRRGGRRGAGLVLGALLGAGLAVGASASBYDVSFQSDIGPVQSGRPFYKPPQCV 60  
DB 60 MGIGRSRRGGRRG-ALGVLAAGLAVGASASBYDVSFQSDIGPVQSGRPFYKPPQCV 59

Query 181 IPADURCHNRYKQWNLPLNLEHETWAKVOQASSWPLANKNCHAGTQVFLCSLFP 120  
DB 60 IPADURCHNRYKQWNLPLNLEHETWAKVOQASSWPLANKNCHAGTQVFLCSLFP 119

Query 121 CDRPRTYPCRMCEAVRDSCFVSPMFGFVPEMLKCDKPPRGDVCTAMTPNATRASKP 180  
DB 120 CDRPRTYPCRMCEAVRDSCFVSPMFGFVPEMLKCDKPPRGDVCTAMTPNATRASKP 179

Query 181 OGTTVCPDCNLSKSAIIEHICASFALRMKICKEVKGENDKKIVPKKKPLKLGPIK 240  
DB 180 OGTTVCPDCNLSKSAIIEHICASFALRMKICKEVKGENDKKIVPKKKPLKLGPIK 239

Query 241 KDLKKGVLYLKNGADCPCHQDNLSHFLIMGRKVQSOYLTIAHNDKONKEPKFNMKK 300  
DB 240 KDLKKGVLYLKNGADCPCHQDNLSHFLIMGRKVQSOYLTIAHNDKONKEPKFNMKK 299

Query 301 MKNHECPTFQSVFK 314  
DB 300 MKNHECPTFQSVFK 313

RESULT 3  
US-09-949-016-6299  
; Sequence 2, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CJU01307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIORITY APPLICATION NUMBER: 60/241,755  
PRIORITY FILING DATE: 2000-10-20  
PRIORITY APPLICATION NUMBER: 60/237,768  
PRIORITY FILING DATE: 2000-10-03  
PRIORITY APPLICATION NUMBER: 60/231,498  
PRIORITY FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 707012  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 6299  
LENGTH: 313  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-6299

Query Match 99.2%; Score 1691.5; DB 2; Length 313;  
Best Local Similarity 99.7%; Pred. No. 3.6e-13; Matches 313; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
Matches 313; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query 1 MGIGRSRRGGRRGAGLVLGALLGAGLAVGASASBYDVSFQSDIGPVQSGRPFYKPPQCV 60  
DB 1 MGIGRSRRGGRRG-ALGVLAAGLAVGASASBYDVSFQSDIGPVQSGRPFYKPPQCV 59

Query 61 IPADRURCHNRYKQWNLPLNLEHETWAKVOQASSWPLANKNCHAGTQVFLCSLFP 120  
DB 60 IPADRURCHNRYKQWNLPLNLEHETWAKVOQASSWPLANKNCHAGTQVFLCSLFP 119

Query 121 CDRPRTYPCRMCEAVRDSCFVSPMFGFVPEMLKCDKPPRGDVCTAMTPNATRASKP 180  
DB 120 CDRPRTYPCRMCEAVRDSCFVSPMFGFVPEMLKCDKPPRGDVCTAMTPNATRASKP 179

Query 181 OGTTVCPDCNLSKSAIIEHICASFALRMKICKEVKGENDKKIVPKKKPLKLGPIK 240  
DB 180 OGTTVCPDCNLSKSAIIEHICASFALRMKICKEVKGENDKKIVPKKKPLKLGPIK 239

Query 241 KDLKKGVLYLKNGADCPCHQDNLSHFLIMGRKVQSOYLTIAHNDKONKEPKFNMKK 300  
DB 240 KDLKKGVLYLKNGADCPCHQDNLSHFLIMGRKVQSOYLTIAHNDKONKEPKFNMKK 299

Query 301 MKNHECPTFQSVFK 314  
DB 300 MKNHECPTFQSVFK 313

RESULT 4  
US-09-546-043-3  
; Sequence 3, Application US/09546043  
; Patent No. 6600018  
; GENERAL INFORMATION:  
; APPLICANT: Rubin, Jeffery et al.  
; TITLE OF INVENTION: SECRETED FRIZZLED RELATED PROTEIN, sFRP, FRAGMENTS AND METHODS OF USE THEREOF  
FILE REFERENCE: 53990  
CURRENT APPLICATION NUMBER: US/09/546,043  
CURRENT FILING DATE: 2000-04-10  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 313  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-546-043-3

Query Match 97.2%; Score 1657.5; DB 2; Length 313;  
Best Local Similarity 97.5%; Pred. No. 1.6e-169; Matches 306; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

XX  
PT New secreted Frizzled-related protein-1-binding peptide, for enhancing or  
PT stimulating osteoclast differentiation or to modify T-cell activity in a  
PT subject with e.g. abnormal bone remodeling, achondroplasia or  
PT osteopetrosis.  
XX  
PS Example; Page 74-75; 81pp; English.

CC The invention relates to a purified peptide that binds to secreted  
CC Frizzled-related protein (sFRP)-1. The peptide is useful for enhancing or  
CC stimulating osteoclast differentiation, or to modify T-cell activity in a  
CC subject with abnormal bone remodeling, achondroplasia, Albright's  
CC osteopetrosis. The sFRP-1 is useful for inhibiting  
CC osteoclast formation in a subject with a bone disorder or unwanted bone  
CC resorption, e.g. postmenopausal osteoporosis, Paget's disease, lytic bone  
CC metastases, multiple myeloma, rheumatoid arthritis, orthopercalcemia of  
CC malignancy. Modulating T-cell activity is useful in subjects suspected of  
CC having toxic shock, sepsis, graft-versus-host reactions or acute  
CC inflammatory reactions. The immunostimulatory sFRP-1 binding peptide is  
CC useful in activating the immune system against bacterial, viral and  
CC parasitic infections, and in the treatment of human immunodeficiency  
CC virus (HIV). The present sequence represents a human sFRP-1 netrin  
CC homology domain  
XX

SQ Sequence 141 AA;

Query Match 100.0%; Score 78; DB 5; Length 141;  
Best Local Similarity 100.0%; Pred. No. 0.00046;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Or 1 KKEENGDKKIVPKKKK 15  
52 KKENGDKKIVPKKKK 66

RESULT 2  
AY48493

ID AY48493 standard; protein; 148 AA.  
XX  
AC AY48493;  
XX

DT 08-DBC-1999 (First entry)

XX Human breast tumour-associated protein 38.

XX Expressed sequence tag; EST; human; breast; cancer; cytostatic;  
KW medicaments; gene therapy; treatment; fat metabolism.

OS Homo sapiens.

XX AY48493 standard; protein; 148 AA.

XX Human breast tumour-associated protein 38.

XX Expressed sequence tag; EST; human; breast; cancer; cytostatic;

KW medicaments; gene therapy; treatment; fat metabolism.

XX Human nucleic acid sequences and protein products from normal breast

XX tissue, useful for breast cancer therapy.

XX Claim 28, 175, 206pp; German.

CC This invention describes novel human nucleic acid sequences from normal  
CC breast tissue which have cytostatic activity. The nucleic acid sequences  
CC can be used to produce and isolate full-length gene sequences. They can

CC be used to express proteins, which can be used as tools to find an  
CC activity against breast cancer. The sequences can be used in sense or  
CC antisense form. They are especially useful for medicaments for gene  
CC therapy to treat breast cancer and for treating illnesses associated with  
CC fat metabolism. AAY48493-Y4539 represent protein fragments encoded by  
CC the expressed sequence tags described in the method of the invention  
XX

SQ Sequence 148 AA;

Query Match 100.0%; Score 78; DB 2; Length 148;  
Best Local Similarity 100.0%; Pred. No. 0.00048;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Or 1 KKEENGDKKIVPKKKK 15  
51 KKENGDKKIVPKKKK 65

RESULT 3  
ADR09139

ID ADR09139 standard; protein; 178 AA.  
XX  
AC ADR09139;  
XX

DT 04-NOV-2004 (first entry)

XX Human protein useful for treating neurological disease Seq 2645.  
XX

KW human; oligo-capping method; diagnostic marker; gene therapy;  
KW osteoporosis; neurological disease; Alzheimer's disease;  
KW Parkinson's disease; dementia; short memory; cancer;  
KW sense or motor function; emotional reaction; fear response; panic;  
KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;  
KW tranquiliser.

XX Homo sapiens.

XX EP1447413-A2.

DN 18-AUG-2004.

PP 12-FEB-2004; 2004EP-00003145.

PR 14-FEB-2003; 2003JP-00102207.

PR 09-MAY-2003; 2003JP-00131452.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;  
PI Wakamatsu A, Ishii S, Nagai K, Irie R;  
XX DR WPI; 2004-583265/57.

DR N-PSDB; ADR07183.

XX PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's disease, dementia and various cancers.  
XX

PR Claim 1; SEQ ID NO 2645; 268pp; English.

XX This invention relates to novel, isolated full length human cDNA  
CC molecules and the encoded protein thereof. Specifically, it refers to  
CC cDNA clones obtained by an oligo-capping method, where none of these  
CC clones are identical to any known human mRNAs. The present invention  
CC describes an immunoassay to identify agonists and antagonists, as well as  
CC antibodies, antisense molecules and siRNAs that can all be used to bind  
CC to and modulate expression of the cDNA molecules. As such, these  
CC molecules are useful for diagnostic markers or therapeutic targets for  
CC the various diseases or morbid states. In particular, they are useful in  
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's  
CC disease, Parkinson's disease, dementia, short memory and various cancers,  
CC as well as for maintaining equilibrium of sense or motor function, and  
CC for treating emotional reaction, fear response and panic. Accordingly,  
CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,

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OM protein - protein search, using SW model

Run on: May 5, 2006, 13:50:51 ; Search time 229 seconds

(without alignment) 96.7406 Million cell updates/sec

Title: US-10-666-851-2

perfect score: 1706

Sequence: 1 MGIGRSRRGRRGAALGVLLA.....KNFMKMMKHNHCPTQSVFK 314

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext: 0.5

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05\_80:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1706	100.0	314	1 SFRP1_HUMAN	Q8474 homo sapien
2	1626	95.3	314	2 Q50542_MOUSE	Q50542 mus musculus
3	1623	95.1	314	1 SFRP1_MOUSE	Q8e4u3 mus musculus
4	1607	94.2	308	1 SFRP1_BOVIN	Q91166 bos taurus
5	1489	87.3	314	1 SFRP1_CHICK	Q9qe49 gallus gallus
6	1100.5	64.5	305	2 Q6GZL1_ORVIA	Q6g2k1 oryzis latifolia
7	1092.5	64.0	321	2 Q8KQ33_TETRADON	Q48kx3 tetradon
8	1084	63.9	311	2 Q9Y124_XENLA	Q9y124 xenopus laevis
9	1070.5	62.7	310	2 Q6YMB8_BRARE	Q6yrb8 brachydanio
10	1012	59.3	296	2 Q7T249_BRARE	Q7t2k9 brachydanio
11	955.5	56.0	311	2 Q4R9B2_TEETING	Q4t9b2 tetradon
12	947.5	55.5	281	2 Q5B8J0_BRARE	Q5b8x0 brachydanio
13	946	55.5	315	2 Q6GL50_XENLA	Q6g3j0 xenopus laevis
14	945	55.4	315	2 Q640J3_XENLA	Q640j3 xenopus laevis
15	942.5	55.2	315	2 Q8AMG4_XENLA	Q8awg4 xenopus laevis
16	924.5	54.2	317	1 SFRP2_HUMAN	Q54f47 homo sapien
17	922.5	54.1	314	1 SFRP2_MOUSE	Q9mu66 mus musculus
18	916.5	53.7	315	1 SFRP2_BOVIN	Q9rsc1 bos taurus
19	844	49.5	158	1 SFRP1_RAT	Q9r168 rattus norvegicus
20	718	42.1	178	2 Q6ZSL4_HUMAN	Q6za14 homo sapiens
21	658.5	38.6	295	2 Q6PB8B_XENTR	Q6pb8b xenopus tropicalis
22	649	38.0	295	2 Q4SS00_TEETING	Q4s800 tetradon
23	645.5	37.8	298	2 Q7ZK66_XENLA	Q7zzm6 xenopus laevis
24	629	36.9	282	2 Q8JHC7_BRARE	Q8hc7 brachydanio
25	610	35.8	294	1 SFRP2_CANPA	Q863h1 canis familiaris
26	610	35.8	365	2 Q4H205_CLOON	Q4h2u5 ciona intestinalis
27	605.5	35.5	292	1 SFRP2_CHICK	Q9ta55 gallus gallus
28	605.5	35.5	295	1 SFRP2_MOUSE	Q97299 mus musculus
29	602	35.3	295	1 SFRP2_HUMAN	Q96h11 homo sapiens
30	595.5	34.9	283	2 Q9BG86_RABIT	Q9q986 oryctolagus cuniculus
31	541.5	31.7	2	2 Q42397_CHICK	Q42397 gallus gallus

#### ALIGNMENTS

32	515	30.2	300	2 Q6F2E8_XENTR	Q6f2e8 xenopus tropicalis
33	508.5	29.8	295	2 Q9I897_XENTLA	Q9i897 xenopus laevis
34	463	27.1	293	2 Q41AU4_COIN	Q41au4 ciona intestinalis
35	433	25.4	281	2 Q902G8_BRARE	Q902g8 brachydanio
36	413	24.2	281	2 Q73821_XENTLA	Q73821 xenopus laevis
37	412	24.2	130	2 Q52K37_CHICK	Q52k37 gallus gallus
38	409.5	24.0	280	2 Q9IAU5_XENTLA	Q9iau5 xenopus laevis
39	395	23.2	282	2 Q48S17_TESTING	Q48s17 tetradon
40	392.5	23.0	284	2 Q902A6_ANEMBR	Q902a6 anemone
41	390.5	22.9	261	2 Q61U61_CLEBR	Q61u61 caenorhabditis elegans
42	385	22.6	260	2 Q5GFF5_CHEBL	Q5gff5 caenorhabditis elegans
43	369.5	21.7	282	2 Q7SX78_BRABR	Q7sx78 brachydanio
44	369.5	21.7	289	2 Q504J9_BRABR	Q504j9 brachydanio
45	295	17.3	592	1 Q57328_gallus_gallus	Q57328 gallus gallus

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GenCore version 5.1.7

Biocceleration Ltd.

OM protein - protein search, using SW model

Run on:

May 5, 2006, 13:54:06 ; Search time 39 Seconds

(without alignments)

Title: US-10-666-851-2  
Perfect score: 1706  
Sequence: 1 MGIGRSRRGAGLVLIA..... KNFMKMMKHNBCPTQSVPK 314

Scoring table: BLASTN62  
Gapop 10.0 , Gapext: 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.0+\*

1: pir1+\*  
2: pir2+\*  
3: pir3+\*  
4: pir4+\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query Length DB ID

#### Description

RESULT 1  
J80175  
frizzled protein-1b - human  
C.Species: Homo sapiens (human)  
C.Date: 03-Jul-1998 #sequence\_revision 10-Jul-1998 #text\_change 09-Jul-2004  
C.Accession: J80175  
R.Hu, B.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.  
Biochem. Biophys. Res. Commun. 247, 287-293, 1998

A.Title: Tissue restricted expression of two human frzb in preadipocytes and pancreas  
A.Reference number: J80174; MUID: 98308108; PMID: 962118  
A.Accession: J80175  
A.Molecule type: mRNA  
A.Residues: 1-317 <HUMAN>

A.Cross-references: UNIPROT:014780; UNIPARC:UPI000158811  
A.Genetics: hrr1b

A.Map position: SqI4.3-q12.1  
Query Match 53.8%; Score 917.5; DB 2; Length 317;  
Best Local Similarity 56.3%; Pred. No. 5e-69; Indels 9; Gaps 6;

Matches 178; Conservative 51; Mismatches 78; Indels 9; Gaps 6;

QY 1 MGIGRSRRGAGLVLIA..... KNFMKMMKHNBCPTQSVPK 60  
Dp 1 MRAAAMAGGVTALLI-LGALHAWPARCERYHYQWQAB-PLH-GRSVSKPPGCD 55  
3 276.5 16.2 574 2 J80339  
4 273.5 16.0 568 2 T25162  
5 271.5 15.9 537 2 J80337  
6 265 15.5 647 2 S05540  
7 264 15.5 581 2 S05540  
8 258 15.1 565 2 J80338  
9 256.5 15.0 581 2 J80706  
10 232.5 14.8 641 2 A47054  
11 237.5 13.9 550 2 T37325  
12 228.5 13.4 694 2 S71786  
13 223.5 13.1 197 2 JC7735  
14 221.5 12.6 666 2 JC7712  
15 215 12.5 705 2 J80164  
16 201 11.8 605 2 T31690  
17 201 11.3 1113 2 J80315  
18 170.5 10.0 1774 2 B56101  
19 133.5 7.8 526 2 T13484  
20 132.5 7.8 579 2 JC7629  
21 125 7.3 793 2 JCS539  
22 107.5 6.3 549 2 B86337  
23 97 5.7 785 2 S46672  
24 97 5.7 2228 2 T14029  
25 96.5 5.7 1024 2 S71804  
26 96.5 5.7 1150 2 T15277  
27 93.5 5.5 1474 2 D88550  
28 92.5 5.5 527 1 SAHUF 1051  
29 92.5 5.4 1051 1 JC4091

#### ALIGNMENTS

hypothetical prote  
epidermal growth f  
hypothetical prote  
hypothetical prote  
epidermal growth f  
gag-pro-pol polypr  
ATP-dependent DNA  
hypothetical prote  
TIP1 protein - mou  
transcription fact  
filamentous hemagg  
hypothetical prote  
restriction modifi  
complement compone  
sodium-glucose cot  
G9a protein - huma

30 91 5.3 260 2 T01837  
31 91 5.3 527 2 A42032  
32 91 5.3 1008 2 C84679  
33 91 5.3 1077 2 T21800  
34 91 5.3 1223 1 TVERLV  
35 90.5 5.3 1751 2 T03394  
36 89.5 5.2 792 2 A70476  
37 88 5.2 718 2 T51488  
38 88 5.2 1051 2 S55259  
39 87.5 5.1 1097 2 A56138  
40 87.5 5.1 4152 2 T31102  
41 87.5 5.1 4919 2 T31105  
42 87.5 5.1 578 2 C6452  
43 87 5.1 1699 2 T14074  
44 86.5 5.1 623 2 A49112  
45 86.5 5.1 1001 2 S30385

RESULT 2  
J80174  
frizzled protein-2 - human

C.Species: Homo sapiens (human)  
C.Date: 03-Jul-1998 #sequence\_revision 10-Jul-1998 #text\_change 09-Jul-2004

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GenCore version 5.1.7

### OM protein - protein search, using sw model

Run on: May 5, 2006, 13:50:11 ; Search time 186 Seconds  
(without alignments)

741.747 Million cell updates/sec

Title: US-10-666-851-2

Perfect score: 1706

Sequence: MGIGRSECRRGALGVLIA.....KNPFMKKOMKNNHBCPTFQSVFK 314

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqb, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_21:\*

1: geneseq1980a:\*

2: geneseq1990b:\*

3: geneseq2000b:\*

4: geneseq2001b:\*

5: geneseq2002a:\*

6: geneseq2003ab:\*

7: geneseq2003ba:\*

8: geneseq2004ab:\*

9: geneseq2005b:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

RESULT 1

AAW88528 standard; protein; 314 AA.

AAW88528;

11-MAR-1999 (first entry)

Human Frizzled-related protein (FRP).

FRP; frizzled-related protein; human; Wnt binding domain; recombinant;

cytokine; cell growth; differentiation; migration; tumour suppressor;

oncogenesis; cancer; Drosophila; Wingless protein; Wnt; neoplasia;

KW transgenic; therapeutic.

XX Homo sapiens.

XX

Key

Location/Qualifiers

FT

Peptide

1..28

/note= "putative signal sequence"

FT

Mis-difference

14

/note= "encoded by a CAG insertion sequence observed in

some cDNA constructs"

FT

Protein

29..314

/note= "mature protein"

FT

Domain

57..166

/note= "Wnt binding domain"

FT

Modified-site

173..175

/note= "Asn is potentially N-glycosylated"

FT

Modified-site

263..265

/note= "Asn is potentially N-glycosylated"

FT

FT

PN

W09854325-A1.

XX

XX

PD

03-DRC-1998.

XX

PF

29-MAY-1998;

98W0-US010974.

XX



GenCore Version 5.1.7									
Copyright (c) 1993 - 2006 Bioceleration Ltd.									
Om protein - protein search, using bw model									
Run on:	May 5, 2006, 13:59:41	:	Search time 164 Seconds						
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Perfect score:	17056		799.990 Million cell updates/sec						
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Scoring table:	BLOSUM62								
GapPp 10.0 , Gapext 0.5									
Searched:	1867569 seqs, 417829326 residues								
Total number of hits satisfying chosen parameters:	1867569								
Minimum DB seq length:	0								
Maximum DB seq length:	200000000								
Post-processing: Minimum Match 0%									
Maximum Match 100%									
Listing first 45 summaries									
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	4: /cgn2_6/ptodata/1/puppa/US10A_PUBCOMB.pep:*								
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Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
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2	1706	100.0	314	4	US-10-666-851-2	US-10-666-851-2	Sequence 2, Appl		
3	1706	100.0	314	4	US-10-788-792-148	US-10-788-792-148	Sequence 148, Appl		
4	1701	99.7	314	4	US-10-146-474-7	US-10-146-474-7	Sequence 7, Appl		
5	1701	99.7	314	4	US-10-756-149-5611	US-10-756-149-5611	Sequence 7, Appl		
6	1701	99.7	314	5	US-10-796-008-2	US-10-796-008-2	Sequence 5, Appl		
7	1691.5	99.2	313	4	US-10-138-434A-4	US-10-138-434A-4	Sequence 4, Appl		
8	1691.5	99.2	313	4	US-10-666-851-7	US-10-666-851-7	Sequence 4, Appl		
9	1691.5	99.2	313	4	US-10-146-474-7	US-10-146-474-7	Sequence 4, Appl		
10	1691.5	99.2	313	4	US-10-786-720-43	US-10-786-720-43	Sequence 4, Appl		
11	1691.5	99.2	313	5	US-10-87-525-2	US-10-87-525-2	Sequence 5, Appl		
12	1691.5	99.2	313	5	US-10-847-972-77	US-10-847-972-77	Sequence 5, Appl		
13	1657.5	97.2	313	4	US-10-422-586-3	US-10-422-586-3	Sequence 4, Appl		
14	1657.5	97.2	313	4	US-10-466-136-4	US-10-466-136-4	Sequence 4, Appl		
15	1657.5	97.2	313	4	US-10-425-586-4	US-10-425-586-4	Sequence 4, Appl		
16	1657.5	97.2	313	4	US-10-466-136-4	US-10-466-136-4	Sequence 4, Appl		
17	1623	95.1	314	5	US-10-847-972-80	US-10-847-972-80	Sequence 5, Appl		
18	1267.5	74.3	267	4	US-10-466-136-7	US-10-466-136-7	Sequence 7, Appl		
19	1267.5	74.3	267	4	US-10-466-136-7	US-10-466-136-7	Sequence 7, Appl		
20	1171	68.6	246	4	US-10-425-586-6	US-10-425-586-6	Sequence 6, Appl		
21	1171	68.6	246	4	US-10-466-136-6	US-10-466-136-6	Sequence 6, Appl		
22	971	56.9	229	4	US-10-425-586-8	US-10-425-586-8	Sequence 8, Appl		
23	971	56.9	229	4	US-10-466-136-8	US-10-466-136-8	Sequence 8, Appl		
24	924.5	54.2	317	4	US-10-146-474-6	US-10-146-474-6	Sequence 6, Appl		
25	924.5	54.2	317	4	US-10-338-604-2	US-10-338-604-2	Sequence 2, Appl		
26	54.2	317	4	US-10-330-764-6	US-10-330-764-6	Sequence 6, Appl			
27	54.2	317	5	US-10-768-566-1	US-10-768-566-1	Sequence 1, Appl			
ALIGNMENTS									
RESULT 1									
US-10-138-434A-3									
Sequence 3, Appl									
Publication No. US20030175864A1									
GENERAL INFORMATION:									
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES									
APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES									
APPLICANT: Rubin, Jeffrey S.									
APPLICANT: Finch, Paul									
APPLICANT: Aaronson, Stuart									
APPLICANT: He, Xi									
APPLICANT: He, Xi									
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN FRP AND FRAGMENTS THEREOF									
FILE REFERENCE: 4229-62220									
CURRENT FILING DATE: 2002-05-03									
PRIOR APPLICATION NUMBER: US/10/138,434A									
PRIOR FILING DATE: 1997-05-29									
PRIOR APPLICATION NUMBER: US 60/ 050,417									
PRIOR APPLICATION NUMBER: US 60/ 050,417									
PRIOR FILING DATE: 1997-05-29									
NUMBER OF SEQ ID NOS: 27									
SEQ ID NO 3									
LENGTH: 314									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-10-138-434A-3									
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Best Local Similarity	100.0%	Pred.	No.	8.9e-159;					
Matches	314;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Organism	Homo sapiens								
US-10-138-434A-3									
Query Match	100.0%	Score	1706	DB	4;				
Best Local Similarity	100.0%	Pred.	No.	8.9e-159;					
Matches	314;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Organism	Homo sapiens								
QY	1	MGIGRSSEGGRGAAIGVLA.....KNTMKMKMKHCTPQSFK	314	QY	1	MGIGRSSEGGRGAAIGVLA.....KNTMKMKMKHCTPQSFK	314	QY	1
Db	1	MGIGRSSEGGRGAAIGVLA.....KNTMKMKMKHCTPQSFK	314	Db	1	MGIGRSSEGGRGAAIGVLA.....KNTMKMKMKHCTPQSFK	314	Db	1
QY	61	1 PADYLCHNQYKVNLLNLTMRVQKQDSWPLNKKHAGTOVFLCSLRPV	120	QY	61	1 PADYLCHNQYKVNLLNLTMRVQKQDSWPLNKKHAGTOVFLCSLRPV	120	QY	61
Db	61	1 PADYLCHNQYKVNLLNLTMRVQKQDSWPLNKKHAGTOVFLCSLRPV	120	Db	61	1 PADYLCHNQYKVNLLNLTMRVQKQDSWPLNKKHAGTOVFLCSLRPV	120	Db	61
QY	181	QGTTVCPDPNKLSEALTEHLCASBFAIRMKKKEVKCENGDKK1VPGKKKKJLGPTRK	240	QY	181	QGTTVCPDPNKLSEALTEHLCASBFAIRMKKKEVKCENGDKK1VPGKKKKJLGPTRK	240	QY	181
Db	181	QGTTVCPDPNKLSEALTEHLCASBFAIRMKKKEVKCENGDKK1VPGKKKKJLGPTRK	240	Db	181	QGTTVCPDPNKLSEALTEHLCASBFAIRMKKKEVKCENGDKK1VPGKKKKJLGPTRK	240	Db	181
QY	241	KDLKLUVLYLNGADCPCHOLDNLSHFLIMGRKVSQYLLTAHKDKRKEPKNEMRK	300	QY	241	KDLKLUVLYLNGADCPCHOLDNLSHFLIMGRKVSQYLLTAHKDKRKEPKNEMRK	300	QY	241

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OM protein - protein search, using sw model

Run on: May 5, 2006, 13:58:01 ; Search time 46 Seconds  
 (without alignments)  
 560.351 Million cell updates/sec

Title: US-10-666-851-2  
 Perfect score: 1706  
 Sequence: 1 MGICRSEGRGAGLGVIA.....KNFKKKMNHECPTFQSVFK 314

Scoring table: BLOSUM62  
 Gapop 10.0 , Gpext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:  
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 5: /cgn2\_6/ptodata/1/iaa/RR\_COMB.pep: \*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep: \*

Pred. No. 18 is the number of result predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1701	99.7	314	2 US-08-937-067-7
2	1691.5	99.2	313	2 US-09-514-885-1
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4	1657.5	97.2	313	2 US-09-546-043-3
5	1657.5	97.2	338	2 US-09-546-043-4
6	1629	95.5	314	2 US-09-087-0318-3
7	1614.5	94.6	313	2 US-09-087-0318-4
8	1267.5	74.3	267	2 US-09-546-043-7
9	1171	68.6	246	2 US-09-546-043-6
10	971	56.9	229	2 US-09-546-043-8
11	924.5	54.2	317	2 US-08-937-067-6
12	924.5	54.2	317	2 US-09-949-016-6300
13	911.5	53.4	305	2 US-09-949-016-7706
14	887.5	52.0	195	2 US-09-546-043-5
15	605.5	35.5	295	2 US-09-999-833A-415
16	598	35.1	295	2 US-09-999-833A-415
17	598	35.1	295	2 US-10-020-45A-415
18	597	35.0	295	2 US-09-148-545-179
19	597	35.0	295	2 US-09-621-011-179
20	597	35.0	296	2 US-09-148-545-237
21	597	35.0	296	2 US-09-621-011-237
22	594	34.8	109	2 US-09-087-0318-19
23	508.5	29.8	295	2 US-09-893-654B-6
24	436	25.6	212	2 US-08-937-067-4
25	409.5	24.0	280	2 US-08-893-654B-4
26	387	22.7	281	2 US-08-893-654B-2
27	20.7	113	2 US-09-087-0318-24	

RESULT 1  
 US-08-937-067-7  
 Sequence 7, Application US/08937067  
 Patent No. 6433155

GENERAL INFORMATION:

APPLICANT: Umaneky, Samuel  
 ADDRESS: MORRISON & FOERSTER  
 STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304-1018

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,067  
 FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lehmarc, Susan K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600  
 TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 314 amino acids  
 TYPE: amino acid  
 STRANDBNESS: single  
 TOPOLOGY: linear

US-08-937-067-7

Query Match 99.7%; Score 1701; DB 2; Length 314;  
 Best Local Similarity 99.7%; Prod. No. 3.5e-174;  
 Matches 313; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGICRSEGRGAGLGVIA.....KNFKKKMNHECPTFQSVFK 60  
 Db 1 MGICRSEGRGAGLGVIA.....KNFKKKMNHECPTFQSVFK 60

Om Protein - protein search, using sw model						
Copyright (c) 1993 - 2006 Bioceleration Ltd.						
GenCore version 5.1.7						
Title:	US-10-666-851-2_COPY_217_231	Perfect score:	78	Sequence:	1 XKGENDKKEKIVPKKKK 15	Run on: May 5, 2006, 14:09:22 ; Search time 29 seconds (without alignments)
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	2: /cgn2_6/ptodata/1/1iaa/6_COMB.pep:*					
	3: /cgn2_6/ptodata/1/1iaa/1PCUS_COMB.pep:*					
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3	78	100.0	313	2 US-09-087-031E-4	Sequence 4, Appli	75
4	78	100.0	313	2 US-09-546-043-3	Sequence 3, Appli	76
5	78	100.0	313	2 US-09-514-885-1	Sequence 1, Appli	77
6	78	100.0	313	2 US-09-949-016-6299	Sequence 6299, AP	78
7	78	100.0	314	2 US-08-937-067-7	Sequence 7, Appli	79
8	78	100.0	314	2 US-08-937-031E-3	Sequence 3, Appli	80
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15	45	57.7	318	2 US-09-206-551-46	Sequence 46, Appli	87
16	44	56.4	324	2 US-09-248-796A-16963	Sequence 16963, A	88
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18	43	55.1	316	2 US-09-270-767-34052	Sequence 34052, A	90
19	43	55.1	316	2 US-09-270-767-42269	Sequence 49269, A	91
20	42.5	54.5	106	2 US-09-513-999C-6072	Sequence 6072, AP	92
21	42	53.8	177	2 US-09-621-976-3338	Sequence 3938, AP	93
22	42	53.8	824	2 US-09-248-796A-14797	Sequence 14797, A	94
23	42	53.8	1589	4 PCT-07261-11	Sequence 11, Appli	95
24	42	53.8	1663	4 PCT-US93-07261-16	Sequence 16, Appli	96
25	41	52.6	80	2 US-09-107-532A-8859	Sequence 3859, AP	97
26	41	52.6	109	2 US-09-198-452A-130	Sequence 130, AP	98
27	41	52.6	117	2 US-09-438-185A-114	Sequence 114, AP	99

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Sequence 910535, A	Sequence 91035, A	Sequence 7, Appl
Sequence 919434, Ap	Sequence 919434, Ap	Sequence 8, Appl
Sequence 700, Ap	Sequence 700, Ap	Sequence 9, Appl
Sequence 130, Ap	Sequence 130, Ap	Sequence 10, Appl
Sequence 114, Ap	Sequence 114, Ap	Sequence 11, Appl
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Sequence 2, Appl	Sequence 2, Appl	Sequence 13, Appl
Sequence 27, Appl	Sequence 27, Appl	Sequence 14, Appl
Sequence 27, Appl	Sequence 27, Appl	Sequence 15, Appl
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Sequence 2, Appl	Sequence 2, Appl	Sequence 18, Appl
Sequence 24, Appl	Sequence 24, Appl	Sequence 19, Appl
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Sequence 4, Appl	Sequence 4, Appl	Sequence 25, Appl
Sequence 6, Appl	Sequence 6, Appl	Sequence 26, Appl
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Sequence 9, Appl	Sequence 9, Appl	Sequence 34, Appl
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Sequence 192, Ap	Sequence 192, Ap	Sequence 39, Appl
Sequence 193, Ap	Sequence 193, Ap	Sequence 40, Appl
Sequence 9, Appl	Sequence 9, Appl	Sequence 41, Appl
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Sequence 9, Appl	Sequence 9, Appl	Sequence 43, Appl
Sequence 11, Appl	Sequence 11, Appl	Sequence 44, Appl
Sequence 7, Appl	Sequence 7, Appl	Sequence 45, Appl
Sequence 1, Appl	Sequence 1, Appl	Sequence 46, Appl
Sequence 9, Appl	Sequence 9, Appl	Sequence 47, Appl
Sequence 3, Appl	Sequence 3, Appl	Sequence 48, Appl
Sequence 9, Appl	Sequence 9, Appl	Sequence 49, Appl
Sequence 1, Appl	Sequence 1, Appl	Sequence 50, Appl
Sequence 2, Appl	Sequence 2, Appl	Sequence 51, Appl
Sequence 3, Appl	Sequence 3, Appl	Sequence 52, Appl
Sequence 4, Appl	Sequence 4, Appl	Sequence 53, Appl
Sequence 5, Appl	Sequence 5, Appl	Sequence 54, Appl
Sequence 5183, Ap	Sequence 5183, Ap	Sequence 55, Appl
Sequence 21747, Ap	Sequence 21747, Ap	Sequence 56, Appl
Sequence 5184, Ap	Sequence 5184, Ap	Sequence 57, Appl
Sequence 5182, Ap	Sequence 5182, Ap	Sequence 58, Appl
Sequence 57291, A	Sequence 57291, A	Sequence 59, Appl
Sequence 4, Appl	Sequence 4, Appl	Sequence 60, Appl
Sequence 5, Appl	Sequence 5, Appl	Sequence 61, Appl
Sequence 5183, Ap	Sequence 5183, Ap	Sequence 62, Appl
Sequence 21747, Ap	Sequence 21747, Ap	Sequence 63, Appl
Sequence 10, Appl	Sequence 10, Appl	Sequence 64, Appl
Sequence 5823, Ap	Sequence 5823, Ap	Sequence 65, Appl
Sequence 11, Appl	Sequence 11, Appl	Sequence 66, Appl
Sequence 11, Appl	Sequence 11, Appl	Sequence 67, Appl
Sequence 11, Appl	Sequence 11, Appl	Sequence 68, Appl
Sequence 11, Appl	Sequence 11, Appl	Sequence 69, Appl

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OM protein - protein search, using SW model

Run on: May 5, 2006, 14:10:16 ; Search time 12 seconds  
 (without alignments)  
 57.856 Million cell updates/sec

Title: US-10-666-851-2\_COPY\_217\_231  
 Perfect score: 78  
 Sequence: 1 KKENGDKKVPKKK 15

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext: 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 500 summaries

Database : Published Applications AA\_New:\*

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2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep:\*

3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep:\*

4: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pep:\*

5: /SIDSS/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

6: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pep:\*

7: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep:\*

8: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep:\*

9: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pepl:\*

10: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep:\*

11: /SIDSS/ptodata/1/pubpaa/US60 NEW PUB.pep:\*

12: /SIDSS/ptodata/1/pubpaa/US60 NEW PUB.pep:\*

Result No. Score Query Match Length DB ID Description

1 78 100.0 413 9 US-10-821-234-989 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
 Sequence 999, App  
 Sequence 21505, App  
 Sequence 21504, App  
 Sequence 951, App  
 Sequence 3034, App  
 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

2 43.5 55.9 502 11 US-11-087-99-8879 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
 Sequence 999, App  
 Sequence 21505, App  
 Sequence 21504, App  
 Sequence 951, App  
 Sequence 3034, App  
 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

3 42 53.8 189 11 US-11-189-298-6518 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
 Sequence 999, App  
 Sequence 21505, App  
 Sequence 21504, App  
 Sequence 951, App  
 Sequence 3034, App  
 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

4 42 53.8 500 9 US-10-517-151-4 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
 Sequence 999, App  
 Sequence 21505, App  
 Sequence 21504, App  
 Sequence 951, App  
 Sequence 3034, App  
 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

5 42 53.8 540 11 US-11-087-99-690 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
 Sequence 999, App  
 Sequence 21505, App  
 Sequence 21504, App  
 Sequence 951, App  
 Sequence 3034, App  
 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

6 42 53.8 540 11 US-11-087-99-4162 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
 Sequence 999, App  
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 Sequence 21504, App  
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 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

7 42 53.8 541 11 US-11-087-99-2152 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
 Sequence 999, App  
 Sequence 21505, App  
 Sequence 21504, App  
 Sequence 951, App  
 Sequence 3034, App  
 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

8 41 52.6 263 11 US-11-079-463-8502 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
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 Sequence 21505, App  
 Sequence 21504, App  
 Sequence 951, App  
 Sequence 3034, App  
 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

9 41 52.6 278 11 US-11-079-463-6742 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
 Sequence 999, App  
 Sequence 21505, App  
 Sequence 21504, App  
 Sequence 951, App  
 Sequence 3034, App  
 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

10 41 52.6 375 11 US-11-036-568A-21506 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
 Sequence 999, App  
 Sequence 21505, App  
 Sequence 21504, App  
 Sequence 951, App  
 Sequence 3034, App  
 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

11 41 52.6 409 9 US-10-533-81-1-57 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
 Sequence 999, App  
 Sequence 21505, App  
 Sequence 21504, App  
 Sequence 951, App  
 Sequence 3034, App  
 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

12 41 52.6 472 11 US-11-045-004-999 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
 Sequence 999, App  
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 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

13 41 52.6 474 11 US-11-096-568A-21505 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
 Sequence 999, App  
 Sequence 21505, App  
 Sequence 21504, App  
 Sequence 951, App  
 Sequence 3034, App  
 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

14 41 52.6 544 11 US-11-096-568A-21504 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
 Sequence 999, App  
 Sequence 21505, App  
 Sequence 21504, App  
 Sequence 951, App  
 Sequence 3034, App  
 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

15 41 52.6 545 11 US-11-087-99-951 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
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 Sequence 1839, App  
 Sequence 1, Appli  
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16 41 52.6 547 11 US-11-087-99-3034 Sequence 989, App  
 Sequence 8079, App  
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 Sequence 4, Appli  
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 Sequence 2152, App  
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 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
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 Sequence 951, App  
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 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

17 41 52.6 723 11 US-11-055-00-21506 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
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 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
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 Sequence 57, Appli  
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 Sequence 21505, App  
 Sequence 21504, App  
 Sequence 951, App  
 Sequence 3034, App  
 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

18 40 51.3 35 11 US-11-096-725-1 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
 Sequence 999, App  
 Sequence 21505, App  
 Sequence 21504, App  
 Sequence 951, App  
 Sequence 3034, App  
 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

19 40 51.3 259 11 US-11-079-463-6740 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
 Sequence 999, App  
 Sequence 21505, App  
 Sequence 21504, App  
 Sequence 951, App  
 Sequence 3034, App  
 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

20 40 51.3 611 9 US-10-793-626-2586 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
 Sequence 999, App  
 Sequence 21505, App  
 Sequence 21504, App  
 Sequence 951, App  
 Sequence 3034, App  
 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

21 40 51.3 611 9 US-10-793-626-2586 Sequence 989, App  
 Sequence 8079, App  
 Sequence 6518, App  
 Sequence 4, Appli  
 Sequence 610, App  
 Sequence 4162, App  
 Sequence 2152, App  
 Sequence 8502, App  
 Sequence 6742, App  
 Sequence 21506, App  
 Sequence 57, Appli  
 Sequence 999, App  
 Sequence 21505, App  
 Sequence 21504, App  
 Sequence 951, App  
 Sequence 3034, App  
 Sequence 1839, App  
 Sequence 1, Appli  
 Sequence 6740, App  
 Sequence 8, Appli  
 Sequence 2586, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 12, Appli  
 Sequence 7, Appli  
 Sequence 9, Appli  
 Sequence 11, Appli  
 Sequence 8632, Appli  
 Sequence 25344, Appli  
 Sequence 25726, Appli  
 Sequence 144, Appli  
 Sequence 145, Appli  
 Sequence 25724, Appli  
 Sequence 2071, Appli  
 Sequence 6245, Appli  
 Sequence 1573, Appli  
 Sequence 318, Appli  
 Sequence 8631, Appli  
 Sequence 1611, Appli  
 Sequence 14800, Appli  
 Sequence 2011, Appli  
 Sequence 117, Appli  
 Sequence 118, Appli  
 Sequence 25432, Appli  
 Sequence 1979, Appli  
 Sequence 6738, Appli  
 Sequence 29784, Appli  
 Sequence 2, Appli  
 Sequence 29783, Appli  
 Sequence 29782, Appli  
 Sequence 3443, Appli  
 Sequence 10056, Appli  
 Sequence 11963, Appli  
 Sequence 1067, Appli  
 Sequence 4419, Appli  
 Sequence 4418, Appli  
 Sequence 9706, Appli  
 Sequence 8519, Appli  
 Sequence 975, Appli  
 Sequence 42, Appli  
 Sequence 974, Appli  
 Sequence 973, Appli  
 Sequence 1092, Appli  
 Sequence 1070, Appli  
 Sequence 498, Appli  
 Sequence 1368, Appli  
 Sequence 7169, Appli  
 Sequence 11537, Appli  
 Sequence 34149, Appli  
 Sequence 34148, Appli  
 Sequence 34147, Appli  
 Sequence 32562, Appli  
 Sequence 32561, Appli  
 Sequence 32560, Appli  
 Sequence 17882, Appli  
 Sequence 35, Appli  
 Sequence 36, Appli  
 Sequence 1053, Appli  
 Sequence 1102, Appli  
 Sequence 5820, Appli  
 Sequence 2297, Appli  
 Sequence 205, Appli  
 Sequence 30451, Appli  
 Sequence 30450, Appli  
 Sequence 30449, Appli  
 Sequence 1, Appli  
 Sequence 23, Appli  
 Sequence 627, Appli  
 Sequence 630, Appli  
 Sequence 1024, Appli  
 Sequence 1024, Appli  
 Sequence 1758, Appli  
 Sequence 3937, Appli

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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: May 5, 2006, 14:06:21 ; Search time 38 Seconds

(without alignments)

37.980 Million cell updates/sec

Title: US-10-666-851-2\_COPY\_217\_231

Perfect score: 78

Sequence: 1 KKEENGDKKVVKPKKK 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 Seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%  
Listing first 500 summaries

Database : PIR\_80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No. Score Query Match Length DB ID

Description

hypothetical prote

GenCore version 5.1.7  
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OM protein - protein search, using SW model  
 Run on: May 5, 2006, 14:02:56 ; search time 226 Seconds  
 (without alignments)  
 46.827 Million cell updates/sec

Title: US-10-666-851-2\_COPY\_217\_231  
 Perfect score: 78  
 Sequence: 1 KKENGDKLKVPKKK 15  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext: 0.5

searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 500 summaries

Database : UniProt\_05\_80:\*
 1: uniprot\_sprot:\*
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	78	100.0	158	1 SFRP1_RAT	Q9R168 rattus norv
2	78	100.0	178	2 06ZSL4_HUMAN	Q6z14 homo sapien
3	78	100.0	308	1 SFRP1_BOVIN	Q19116 bov tauris
4	78	100.0	314	1 SFRP1_HUMAN	Q8n74 homo sapien
5	78	100.0	314	1 SFRP1_MOUSE	Q8cu3 mus musculus
6	78	100.0	314	1 SFRP1_MOUSE	Q55a2 mus musculus
7	64	82.1	314	1 SFRP1_CHICK	Q9ddq4 gallus gallus
8	58	74.4	5229	2 Q7RT4_PLAVO	Q7rf4 plasmid
9	51	65.4	536	2 Q6CC4_9ANACH	Q54cc4 uncultured
10	50	64.4	311	2 Q9Y124_XENIA	xenopus lae
11	49	62.8	287	2 Q614B0_CABER	Q614a0 caenorhabditis
12	49	62.8	308	2 Q5YF5_ENTH1	Q5YF5 entamoeba h
13	49	62.8	326	2 Q50QF4_ENTH1	Q50QF4 entamoeba h
14	49	62.8	758	2 Q4RUV9_TEETNG	Q4rui9 tetratodon
15	48	61.5	310	2 Q6YR8_BRABR	Q6YR8 brachydanio
16	48	61.5	321	2 Q4SKK3_TEETNG	Q4skk3 tetratodon
17	47	60.3	297	2 Q82W10_NITR0	Q82w10 nitrosomonas
18	47	60.3	348	2 Q7P5P_PLAVO	Q7p5p plasmid
19	47	60.3	425	2 Q4YPAB_PLAVO	Q4ypa8 plasmid
20	47	60.3	610	2 Q6L1H8_ARATH	Q6l1h8 arabidopsis
21	46	59.0	136	2 Q9W164_9HIV1	Q9w164 human immun
22	46	59.0	261	2 Q4Y8ST_PLAVO	Q4y8st plasmid
23	46	59.0	278	2 Q814L0_CABER	Q814l0 caenorhabditis
24	46	59.0	279	2 Y5T1_GIEEL	Q10033 caenorhabditis
25	46	59.0	286	2 Q909N2_9HIV1	Q909n2 human immun
26	46	59.0	315	2 Q8AWG4_XENIA	Q8awg4 xenopus lae
27	46	59.0	315	2 Q66704_XENIA	Q66704 xenopus lae
28	46	59.0	315	2 Q6GL50_XENIA	Q6gl50 xenopus lae
29	46	59.0	324	2 Q54Q96_DICDB	Q54q96 dictyostelia
30	46	59.0	377	2 Q425H0_PLAVO	Q425h0 plasmid
31	46	59.0	397	1 YXK7_CABEL	Q18674 caenorhabditis

32	46	59.0	441	2 Q58EAB_BRABR	Q58eab brachydanio
33	46	59.0	510	2 Q4V7X3_XENLA	Q4v7x3 xenopus lae
34	46	59.0	532	2 Q90W60_XENLA	Q90w60 xenopus lae
35	46	59.0	713	2 Q6PAK0_XENLA	Q6pak0 xenopus lae
36	46	59.0	715	2 Q4882_PLAVO	Q4882 plasmid
37	46	59.0	725	2 Q565B8_ENTH1	Q565b8 entamoeba h
38	46	59.0	819	2 Q54J99_DICDB	Q54j99 dictyostelia
39	46	59.0	912	2 Q6KBR9_9HIV1	Q6kbr9 human immun
40	46	59.0	999	2 Q4G336_9HIV1	Q4g336 human immun
41	46	59.0	1002	2 Q8U8Z3_9HIV1	Q8u8z3 human immun
42	46	59.0	1003	2 Q80B07_GHIV1	Q80b07 human immun
43	46	59.0	1010	2 Q5K6J6_SIVCZ	Q5k6j6 chimpanzee
44	46	59.0	1011	2 Q8TTF1_9HIV1	Q8ttf1 human immun
45	46	59.0	1012	2 Q673V0_9HIV1	Q673v0 human immun
46	46	59.0	1069	2 Q519R3_ENTH1	Q519r3 entamoeba h
47	46	59.0	1080	2 Q510Y4_ENTH1	Q510y4 entamoeba h
48	46	59.0	1431	2 Q8A872_9HIV1	Q8a872 human immun
49	46	59.0	1433	2 Q91E69_9HIV1	Q91e69 human immun
50	46	59.0	1449	2 Q91080_9HIV1	Q91080 human immun
51	46	59.0	1449	2 Q91D0V_9HIV1	Q91d0v human immun
52	46	59.0	18159	2 Q81SP6_CABEL	Q81sp6 arabidopsis
53	46	59.0	18534	2 Q81SP7_CABEL	Q81sp7 arabidopsis
54	45	57.7	65	2 Q34700_BACSU	Q34700 bacillus su
55	45	57.7	84	2 Q7P110_TETNG	Q7p110 tetratodon
56	45	57.7	350	2 Q7RGP6_PLAVO	Q7rgp6 plasmid
57	45	57.7	194	2 Q7VIGS_BORP8	Q7vig8 borodetella
58	45	57.7	418	2 Q7WAB9_ARATH	Q7wab9 arabidopsis
59	45	57.7	493	2 Q7WIB8_BORP8	Q7wib8 borodetella
60	45	57.7	213	2 Q4UHQ9_THERAN	Q4uhq9 therelaria a
61	45	57.7	315	1 Q8P05_BOTIN	Q8p05 botulinus su
62	45	57.7	317	1 Q8P05_HUMAN	Q8p05 human immun
63	45	57.7	350	2 Q7RGP6_PLAVO	Q7rgp6 plasmid
64	45	57.7	418	2 Q4S674_TESTNG	Q4s674 tetratodon
65	45	57.7	574	2 Q55C31_DICDB	Q55c31 dictyosteli
66	45	57.7	577	2 Q7Y2U2_9HIV1	Q7y2u2 human immun
67	45	57.7	630	2 Q4YV70_PLAVO	Q4yv70 plasmid
68	45	57.7	699	2 Q5FXS8_9HIV1	Q5fxs8 human immun
69	45	57.7	714	2 Q7RG16_PLAVO	Q7rg16 plasmid
70	45	57.7	1055	2 Q4YXY6_PLAVO	Q4xyy6 plasmid
71	45	57.7	1089	2 Q75B21_ASHHGO	Q75b21 ashbya gossypii
72	44.5	57.1	289	2 Q4YVFA_PLAVO	Q4yvfa plasmid
73	44.5	57.1	317	2 Q4YV46_PLAVO	Q4yv46 plasmid
74	44.5	57.1	516	2 Q6A141_DICDB	Q6a141 desulfovibrio
75	44	56.4	273	2 Q5A8P8_CANAL	Q5a8p8 canidae alb
76	44	56.4	278	2 Q8D284_WCBR	Q8d284 wiggleswort
77	44	56.4	281	2 Q56X00_BARR	Q56x0 brachydanio
78	44	56.4	296	2 Q7T2K9_BRARKE	Q7t2k9 brachydanio
79	44	56.4	335	2 Q51755_ACYCP1	Q51755 acyrtosiphon
80	44	56.4	377	1 QDNJ_STRT1	Q5n1j7 streptococc
81	44	56.4	377	1 QDNJ_STRT2	Q5n1d0 streptococc
82	44	56.4	476	2 Q4X1L6_PLAVO	Q4x1l6 plasmid
83	44	56.4	502	2 Q20240_CABER	Q20240 caenorhabditis
84	44	56.4	562	2 Q90018_9HIV1	Q90018 sabbia virus
85	44	56.4	562	2 Q59388_CANAL	Q59388 entamoeba h
86	44	56.4	637	2 Q5T8Q0_ANOGA	Q5t8q0 anophelles g
87	44	56.4	659	2 Q6BKNG6_DIBERA	Q6bkng6 debaryomyce
88	44	56.4	690	2 Q7PCN5_ANOGA	Q7pcn5 anophelles g
89	44	56.4	743	2 Q6R1M7_HUMAN	Q6r1m7 homo sapien
90	44	56.4	868	2 Q50316_BRARKE	Q50316 brachydanio
91	44	56.4	919	2 Q70442_ANOGA	Q70442 anophelles g
92	44	56.4	972	2 Q5TSU5_ANOGA	Q5tsu5 anophelles g
93	44	56.4	1003	2 Q69G87_9HIV1	Q69g87 human immun
94	44	56.4	1003	2 Q69G87_9HIV1	Q69g87 human immun
95	44	56.4	1476	2 Q5G824_XENIA	Q5g824 xenopus lae
96	44	56.4	2378	2 Q813J00_PLAVO	Q813j0 plasmid
97	44	56.4	4261	2 Q81FP4_PLAVO	Q81fp4 plasmid
98	43.5	55.8	502	2 Q80303_DICDB	Q80303 dicystosteli
99	43	55.1	61	2 Q81108_PLAVO	Q81108 plasmid
100	43	55.1	120	2 Q95XH4_CABER	Q95xh4 caenorhabditis
101	43	55.1	127	2 Q4J7N1_SUNAC	Q4j7n1 sulfolobus
102	43	55.1	132	2 Q9L259_ARATH	Q9l259 arabidopsis
103	43	55.1	163	2 Q89Y17_ARATH	Q89y17 arabidopsis
104	43	55.1	175	2 Q9SVB4_ARATH	Q9svb4 arabidopsis

OM protein - protein search, using sw model	GenCore version 5.1.7	Copyright (c) 1993 - 2006 Biocceleration Ltd.
Run on:	May 5, 2006, 14:10:03 ; Search time 76 Seconds (without alignments)	82.466 Million cell updates/sec
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Perfect score:	78	4
Sequence:	1 KKGENDKIVPKKK 15	4
Scoring table:	BLOSUM62	4
Searched:	Gapop 10.0 , Gapext 0.5 1867569 seqs, 417829326 residues	4
Total number of hits satisfying chosen parameters:	1867569	4
Minimum DB seq length:	0	4
Maximum DB seq length:	200000000	4
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 500 summaries	4
Database :	Published Applications AA_Main:*	4
1:	/cgn2_6/prodata/1/pupaa/US07_PUBCOMB.pep:*	4
2:	/cgn2_6/prodata/1/pupaa/US08_PUBCOMB.pep:*	4
3:	/cgn2_6/prodata/1/pupaa/US09_PUBCOMB.pep:*	4
4:	/cgn2_6/prodata/1/pupaa/US10_PUBCOMB.pep:*	4
5:	/cgn2_6/prodata/1/pupaa/US10B_PUBCOMB.pep:*	4
6:	/cgn2_6/peodata/1/pupaa/US11_PUBCOMB.pep:*	4
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
	SUMMARIES	
Result No.	Score	Query Match Length DB ID
		----- Description -----
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2	78	100.0 100-15-75-88 Sequence 8, Appli
3	78	100.0 229 4 US-10-456-136-8 Sequence 7, Appli
4	78	100.0 267 4 US-10-425-586-7 Sequence 7, Appli
5	78	100.0 267 4 US-10-425-586-7 Sequence 2, Appli
6	78	100.0 313 3 US-09-756-08-2 Sequence 4, Appli
7	78	100.0 313 4 US-10-138-434-4 Sequence 3, Appli
8	78	100.0 313 4 US-10-425-586-3 Sequence 3, Appli
9	78	100.0 313 4 US-10-466-136-3 Sequence 7, Appli
10	78	100.0 313 4 US-10-666-851-2 Sequence 43, Appli
11	78	100.0 313 5 US-10-817-525-2 Sequence 2, Appli
12	78	100.0 313 5 US-10-847-972-77 Sequence 4, Appli
13	78	100.0 314 4 US-10-847-974-7 Sequence 3, Appli
14	78	100.0 314 4 US-10-425-586-4 Sequence 7, Appli
15	78	100.0 314 4 US-10-301-764-7 Sequence 2, Appli
16	78	100.0 314 4 US-10-666-851-2 Sequence 18, Appli
17	78	100.0 314 4 US-10-789-792-148 Sequence 77, Appli
18	78	100.0 314 5 US-10-847-972-80 Sequence 7, Appli
19	78	100.0 314 5 US-10-755-15-5611 Sequence 3, Appli
20	78	100.0 338 4 US-10-425-586-4 Sequence 4, Appli
21	78	100.0 338 4 US-10-466-136-4 Sequence 7, Appli
22	78	100.0 338 4 US-10-617-320-4788 Sequence 2, Appli
23	78	67.9 108 4 US-10-424-599-210561 Sequence 210561, Appli
24	50.5	64.7 114 4 US-10-425-15-230923 Sequence 230923, Appli
25	50	64.1 83 4 US-10-425-15-231235 Sequence 231235, Appli
26	50	64.1 153 4 US-10-425-15-231235 Sequence 231235, Appli
27	49	62.8 66 4 US-10-425-15-277499 Sequence 277499, Appli
28	48	61.5 78 4 US-10-425-115-243409 Sequence 243409, Appli
29	47	60.3 89 4 US-10-437-963-126220 Sequence 126220, Appli
30	47	60.3 100 4 US-10-425-115-203483 Sequence 203483, Appli
31	47	60.3 105 4 US-10-425-115-238136 Sequence 238136, Appli
32	47	60.3 106 4 US-10-425-115-276508 Sequence 276508, Appli
33	47	60.3 158 4 US-10-425-115-365021 Sequence 365021, Appli
34	47	60.3 165 4 US-10-425-115-207527 Sequence 207527, Appli
35	46.5	59.6 48 4 US-10-425-115-218785 Sequence 218785, Appli
36	46	59.0 82 4 US-10-425-115-201158 Sequence 201158, Appli
37	46	59.0 90 4 US-10-425-115-276281 Sequence 276281, Appli
38	46	59.0 90 4 US-10-425-115-280739 Sequence 280739, Appli
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41	45	57.7 83 4 US-10-425-115-351455 Sequence 351455, Appli
42	45	57.7 91 4 US-10-425-115-197216 Sequence 197216, Appli
43	45	57.7 119 4 US-10-424-599-273759 Sequence 273759, Appli
44	45	57.7 122 4 US-10-425-115-200729 Sequence 200729, Appli
45	45	57.7 184 4 US-10-424-599-188977 Sequence 188977, Appli
46	45	57.7 194 4 US-10-428-112A-510335 Sequence 510335, Appli
47	45	57.7 317 4 US-10-14-6-474-6 Sequence 6, Appli
48	45	57.7 417 4 US-10-338-604-2 Sequence 2, Appli
49	45	57.7 449 4 US-10-301-764-6 Sequence 148923, Appli
50	45	57.7 517 5 US-10-768-566-1 Sequence 1, Appli
51	45	57.7 816 4 US-10-425-115-280739 Sequence 280739, Appli
52	45	57.7 931 4 US-10-425-115-262142 Sequence 262142, Appli
53	45	57.7 1018 4 US-10-424-599-18923 Sequence 18923, Appli
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55	44	56.4 58 4 US-10-425-115-347336 Sequence 347336, Appli
56	44	56.4 63 4 US-10-437-963-124929 Sequence 124929, Appli
57	44	56.4 65 4 US-10-424-599-236334 Sequence 236334, Appli
58	44	56.4 66 4 US-10-424-599-164574 Sequence 164574, Appli
59	44	56.4 66 4 US-10-425-115-208959 Sequence 208959, Appli
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61	44	56.4 71 4 US-10-425-115-28506 Sequence 278506, Appli
62	44	56.4 78 4 US-10-437-963-193907 Sequence 193907, Appli
63	44	56.4 81 4 US-10-425-115-224408 Sequence 224408, Appli
64	44	56.4 84 4 US-10-425-115-362096 Sequence 362096, Appli
65	44	56.4 85 4 US-10-437-963-182779 Sequence 182779, Appli
66	44	56.4 85 4 US-10-767-701-52041 Sequence 52041, Appli
67	44	56.4 114 4 US-10-424-599-150171 Sequence 150171, Appli
68	44	56.4 124 4 US-10-425-115-22125 Sequence 22125, Appli
69	44	56.4 160 4 US-10-425-115-328001 Sequence 328001, Appli
70	44	56.4 202 4 US-10-425-115-255669 Sequence 255669, Appli
71	44	56.4 246 4 US-10-732-923-4505 Sequence 4505, Appli
72	44	56.4 335 5 US-10-732-585-7314 Sequence 7334, Appli
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74	43	55.1 39 4 US-10-425-115-347111 Sequence 347111, Appli
75	43	55.1 40 4 US-10-25-115-234601 Sequence 234601, Appli
76	43	55.1 40 4 US-10-425-115-28895 Sequence 28895, Appli
77	43	55.1 44 4 US-10-425-115-25065 Sequence 25065, Appli
78	43	55.1 49 4 US-10-425-115-196660 Sequence 196660, Appli
79	43	55.1 51 4 US-10-437-963-125118 Sequence 125118, Appli
80	43	55.1 51 4 US-10-425-115-22620 Sequence 22620, Appli
81	43	55.1 59 4 US-10-425-115-192331 Sequence 192331, Appli
82	43	55.1 63 4 US-10-425-115-26445 Sequence 26445, Appli
83	43	55.1 64 4 US-10-425-115-312017 Sequence 312017, Appli
84	43	55.1 70 4 US-10-424-599-213013 Sequence 213013, Appli
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86	43	55.1 76 4 US-10-425-115-35371 Sequence 35371, Appli
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91	43	55.1 92 4 US-10-425-115-25967 Sequence 25967, Appli
92	43	55.1 100 4 US-10-425-115-31626 Sequence 31626, Appli
93	43	55.1 109 4 US-10-425-115-28141 Sequence 28141, Appli
94	43	55.1 110 4 US-10-424-599-22880 Sequence 22880, Appli
95	43	55.1 125 4 US-10-427-963-174885 Sequence 174885, Appli
96	43	55.1 125 4 US-10-425-115-28613 Sequence 28613, Appli
97	43	55.1 144 5 US-10-637-320-3451 Sequence 3451, Appli
98	43	55.1 164 5 US-10-425-115-336291 Sequence 336291, Appli
99	43	55.1 180 4 US-10-427-963-11226 Sequence 11226, Appli
100	43	55.1 184 4 US-10-424-599-16459 Sequence 16459, Appli

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OM protein - protein search, using sw model

Run on: May 5, 2006, 14:02:26 ; Search time 184 seconds  
(without alignments)  
(35.819 Million cell updates/sec)

title: US-10-666-851-2\_COPY\_217\_231  
perfect score: 78  
Sequence: 1 KKENGDKKIVPKKKK 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378761 residues  
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 500 summaries

Database : A\_Geneseq\_21:\*

1: geneseq1980s:\*

2: geneseq2190s:\*

3: geneseq2000s:\*

4: geneseq2001s:\*

5: geneseq2002s:\*

6: geneseq2003ab:\*

7: geneseq2004ab:\*

8: geneseq2005ab:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	% Match	Length	DB ID	Description
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2	78	100.0	148	2	ARY48493	ARY8493 Human bre
3	78	100.0	178	8	ADR09139	Adr09139 Human pro
4	78	100.0	229	5	ABR82249	Abbr2249 Human sec
5	78	100.0	229	7	ADCT7191	Adct7191 Deletion
6	78	100.0	229	8	ADH43313	Adh43313 Human sec
7	78	100.0	267	5	ABR82248	Abbr2248 Human sec
8	78	100.0	267	7	ADCT7190	Adct7190 Deletion
9	78	100.0	267	8	ADH43312	Adh43312 Human sec
10	78	100.0	313	4	AABE0154	Aae0154 Human sec
11	78	100.0	313	4	ARU0695	Aau0695 Human FRI
12	78	100.0	313	5	ABBB2244	Abbb2244 Human sec
13	78	100.0	313	6	ABP72784	Abp72784 Human sec
14	78	100.0	313	7	ABR64428	Abbr64428 Human sec
15	78	100.0	313	7	ADCT71186	Adct71186 Human sec
16	78	100.0	313	8	ADH43308	Adh43308 Human sec
17	78	100.0	313	8	ADP68541	Adp68541 Human sec
18	78	100.0	313	8	ADU86503	Adu86503 Human sec
19	78	100.0	313	8	ADU6566	Adu6566 Human lyp
20	78	100.0	313	9	ADV48410	Adv48410 Secreted
21	78	100.0	313	9	ADX58916	Adx58916 Human reg
22	78	100.0	314	2	AWW82817	Raw7817 Human sec
23	78	100.0	314	2	AWW82828	Raw82828 Human FRI
24	100.0	314	2	ABP72785	Abp72785 Human sec	

ABP72783 Human SFR  
Abp61429 Murine em  
Abp61427 Murine em  
Abp68536 Human sec  
Ad99142 Secreted  
Ad986505 Mouse sec  
Abp82245 Human sec  
Adc71187 Human SFR  
Adb43309 Human SFR  
Adb82799 Human dia  
Adb96153 Novel S  
Aes60023 Streptoco  
Aeo05308 Human pol  
Aeo053108 Human pol  
Aeo055177 Human pol  
Aam12915 Octapepti  
Aeo4686 Human pol  
Adb9977 HIV pol  
Adc39945 HIV pol p  
Adc39998 HIV pol p  
Adc39928 HIV pol p  
Adc40087 HIV pol p  
Aaw68474 HIV-1 str  
Abb23111 Protein e  
Aaw73507 Human ATG  
Aaw37816 Human sec  
Aeo38289 Human sec  
Adm6722 Human hom  
Adp56062 Human PRO  
Aab01769 SIm19 Human im  
Aac02187 Human pol  
Abp73497 Candida a  
Aao02430 Human pol  
Aag14889 Arabidops  
Aao03896 Human pol  
Aag14886 Arabidops  
Adc54915 Novel S  
Aeo38686 Streptoco  
Adc40058 HIV pol p  
Abi8277 Plasmodiu  
Aag01991 Human sec  
Aao03273 Human pol  
Aao2310 Human pol  
Aag5277 Arabidops  
Aao33061 Arabidops  
Ado3137 Human dia  
Abo9159 Human end  
Aag49440 Arabidops  
Aag60974 Arabidops  
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Aag49439 Arabidops  
Aag60973 Arabidops  
Aao02432 Mouse sec  
Adm67241 Murine ad  
Ado3987 Human CDK  
Aam19489 Human pro  
Aam1589 Human pol  
Aam41588 Human pol  
Abb64443 Drosophil  
Abc1549 Human nov  
Aam78505 Human pro  
Aam3943 Human pol  
Aam3943 Human pol  
Abg95660 Human nuc  
Abh44816 Human KRZ  
Adl12095 Human pro  
Adn2640 Bacterial  
Adz2639 Bacterial  
Aam3943 Human pol  
Abm39803 Human pol  
Abm39803 Human pol  
Abm8619 Rice abio  
Abb2593 Rice bicida  
Abm8655 Rice abio  
Abm9383 Rice abio  
Aam9802 Human pol  
Adp99073 C. albica

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OM nucleic - nucleic search, using Bw model

Run on: May 7, 2006, 14:06:06 ; Search time 1173 Seconds  
(without alignments)

903.880 Million cell updates/sec

Title: US-10-666-851-1

Perfect score: 2602

Sequence: 1 gatctgtggggactgcgc.....gaagtatgtctaaaaaaa 2602

Scoring table: IDENTITY\_NUC  
Gapext 10.0, Gapext 1.0

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%, Maximum Match 100%

Listing first 45 summaries

Searched: 9306428 seqs, 203626896 residues

Total number of hits satisfying chosen parameters: 18612856

Sequence 17, APP

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Sequence 25, APP

Published Applications NA New:\*

Sequence 186, APP

Sequence 204, APP

Sequence 23, APP

Sequence 2630, APP

Sequence 6299, APP

Sequence 154, APP

Sequence 21, APP

Sequence 35, APP

Sequence 1, APP

Sequence 5, APP

Sequence 208, APP

Sequence 630, APP

Sequence 1, APP

Sequence 55, APP

Sequence 5, APP

Sequence 2374, APP

Sequence 1, APP

Sequence 1886, APP

Sequence 46, APP

Sequence 57, APP

Sequence 154, APP

Sequence 1, APP

Sequence 5450, APP

RESULT 1  
US-11-245-147-203  
; Sequence 203, Application US/11245147  
; Publication No. US20060030541A1  
; GENERAL INFORMATION:  
; APPLICANT: GARCIA, TERESA  
; APPLICANT: ROMAN, ROMAN, SERGIO  
; APPLICANT: BARON, ROLAND  
; APPLICANT: CALL, KATHERINE  
; APPLICANT: THILHABER, JOACHIM  
; APPLICANT: CONNOLY, TIMOTHY  
; APPLICANT: JACKSON, AMANDA  
; APPLICANT: BUSNELL, STEVEN  
; APPLICANT: RAWADI, GEORGES  
; CURRENT APPLICATION NUMBER: US/11/245,147  
; CURRENT FILING DATE: 2005-10-07  
; PRIORITY APPLICATION NUMBER: PCT/IB02/02211  
; PRIORITY FILING DATE: 2001-04-05  
; NUMBER OF SEQ ID NOS: 245  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO: 203  
; LENGTH: 4469  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Homo sapiens secreted frizzled-related protein 1  
; OTHER INFORMATION: (SFRP1), mRNA.  
; OTHER INFORMATION: (SFRP1), mRNA.  
; OTHER INFORMATION: (SFRP1), mRNA.

## ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result <sup>*</sup>	Score	Query	Length	DB	ID	Description
1	2465.4	94.8	4469	18	US-11-245-147-203	Sequence 203, APP
2	2465.4	94.8	4608	10	US-11-245-147-203	Sequence 137, APP
3	417.4	16.0	475	17	US-11-004-762-19	Sequence 19, APP
4	370.4	14.2	630	12	US-10-301-480-560598	Sequence 560598, APP
5	370.4	14.2	630	12	US-10-301-480-1174007	Sequence 1174007, APP
6	231.4	8.9	926	18	US-11-245-147-5	Sequence 5, APP
7	228	8.8	1382	18	US-11-245-147-197	Sequence 197, APP
8	226.4	8.7	1196	13	US-11-245-147-414	Sequence 414, APP
9	176.6	6.8	1745	18	US-11-051-720-28	Sequence 28, APP
10	164.8	6.3	882	18	US-11-245-147-80	Sequence 80, APP
11	116.6	4.5	2379	7	US-09-925-056-78403	Sequence 678403, APP
12	114	4.4	4350	18	US-11-245-147-124	Sequence 124, APP
13	114	4.4	4350	18	US-11-245-147-105	Sequence 125, APP
14	4.4	4350	18	US-11-245-147-205	Sequence 205, APP	

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OM nucleic - nucleic search, using sw model  
Run on: May 6, 2006, 13:51:57 ; Search time 788 Seconds  
(without alignments)  
5869.563 Million cell updates/sec

Title: US-10-666-851-1

Perfect score: 2602

Sequence: 1 gatctgtggactgcgcc.....gaatgtttctaaaaaaa 2602

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/ina/5\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/6C\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/6CTUS\_COMB.seq: \*  
7: /cgn2\_6/ptodata/1/ina/PP\_COMB.seq: \*  
8: /cgn2\_6/ptodata/1/ina/RB\_COMB.seq: \*  
9: /cgn2\_6/ptodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

#### ALIGNMENTS

RESULT 1  
US-09-087-031B-27  
; Sequence 27, Application US/09087031B  
; Patent No. 6479255  
; GENERAL INFORMATION:  
; APPLICANT: Rubin, Jeffrey S.  
; APPLICANT: Finch, Paul  
; APPLICANT: Axelson, Stuart  
; APPLICANT: He, Xi  
; TITL OF INVENTION: HUMAN FRP AND FRAGMENTS THEREOF INCLUDING METHODS FOR USING THEM  
; FILE REFERENCE: 11613.US11  
; CURRENT APPLICATION NUMBER: US/09/087,031B  
; CURRENT FILING DATE: 1998-01-29  
; PRIORITY NUMBER: 09/087,031  
; PRIORITY DATE: 1998-05-29  
; PRIORITY APPLICATION NUMBER: 60/050,417  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27  
; LENGTH: 4500

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2 2465.4 94.8 4245 3 US-09-0949-016-428 Sequence 428, Appli  
3 2302.8 88.5 2078 3 US-09-276-531-16 Sequence 16, Appli  
4 1803.9 69.3 2075 3 US-09-087-031B-1 Sequence 1, Appli  
5 187.8 68.7 2075 3 US-09-087-031B-2 Sequence 2, Appli  
6 1787.8 68.7 2075 3 US-09-546-043-1 Sequence 1, Appli  
7 1787.8 68.7 2075 3 US-09-514-885-2 Sequence 2, Appli  
8 1621.6 62.3 3360 3 US-09-949-016-312 Sequence 3312, AP  
9 1621.6 62.3 7360 3 US-09-949-016-15054 Sequence 15054, A  
10 1076.2 41.4 1308 3 US-09-937-067-18 Sequence 18, Appli  
11 912.6 35.0 1942 3 US-09-546-043-2 Sequence 2, Appli  
12 909.6 35.0 1017 3 US-09-546-043-9 Sequence 9, Appli  
13 697 69.8 804 3 US-09-546-043-12 Sequence 12, Appli  
14 69.4 74.1 3 US-09-546-043-11 Sequence 11, Appli  
15 603.2 23.2 2124 3 US-09-087-031B-26 Sequence 26, Appli  
C 16 597.4 23.0 601 3 US-09-949-016-28352 Sequence 26352, A  
C 17 597.4 23.0 601 3 US-09-949-016-6353 Sequence 26353, A  
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C 19 597.4 23.0 601 3 US-09-949-016-119369 Sequence 119369, A  
20 18.5 588 3 US-09-546-043-10 Sequence 10, Appli  
21 44.4 17.1 690 3 US-09-546-043-13 Sequence 13, Appli  
C 22 41.1 15.8 601 3 US-09-949-016-28354 Sequence 26354, A  
C 23 41.1 15.8 601 3 US-09-949-016-119370 Sequence 119370, A  
24 401.2 15.4 1905 3 US-09-949-016-429 Sequence 429, Appli

OM nucleic - nucleic search, using sw model	Run on: May 7, 2006, 13:44:04 ; Search time 9249 Seconds (without alignments) 13162.503 Million cell updates/sec	GenCore version 5.1.8 Copyright (c) 1993 - 2006 Biocceleration Ltd.
<b>Title:</b> US-10-666-851-1	<b>Perfect score:</b> 2602	<b>Scoring table:</b> IDENTITY_NUC
<b>Sequence:</b> 1 gatctgctggggactgcgcc.....gaagtagtgtctaaaaaaa 2602	<b>Scoring table:</b> Gapop 10.0 , Gapext 1.0	<b>Searched:</b> 41078325 seqs, 23393541228 residues
<b>Total number of hits satisfying chosen parameters:</b> 82156650	<b>Minimum DB seq length:</b> 0	<b>Maximum DB seq length:</b> 200000000
<b>Post-processing:</b> Minimum Match 0% Maximum Match 100% Listing first 45 summaries	<b>Pred. No.</b> is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
<b>SUMMARIES</b>		
<b>Result No.</b>	<b>Score</b>	<b>Query Match Length DB ID</b>
1	875.6	33.7 2704 4 AK088868
2	803	30.9 891 8 CV810231
3	794.4	30.5 101 5 BII96604
4	762	29.3 837 1 AU131621
5	758.2	29.1 763 8 CX786676
6	757.8	29.1 2298 4 AK01052
7	755.2	29.0 762 7 CM271890
8	744.8	28.6 946 4 BE004466
9	732	28.1 614 6 CD644680
10	731.2	28.1 913 5 BO879583
11	723	803 6 CD616079
12	708.6	27.2 5 BQ932355
13	679.4	26.1 823 1 AU127052
14	676.2	26.0 801 8 CX781693
15	669.5	25.7 722 7 CM271889
16	668	25.7 779 6 CB47875
17	660.2	25.4 741 7 CR769220
18	658.6	25.3 738 5 BO771388
19	647.6	24.9 668 1 AU121566
20	643.8	24.7 647 1 AW57689
21	637.2	24.5 756 6 CD616078
22	633.2	24.3 907 2 BG119546
<b>c</b>	<b>23</b>	<b>633 24.3</b>
	<b>24</b>	<b>624 24.0</b>
	<b>25</b>	<b>618.2 23.8</b>
	<b>25</b>	<b>614.2 23.6</b>
	<b>27</b>	<b>608.2 23.4</b>
	<b>28</b>	<b>606.4 23.3</b>
	<b>29</b>	<b>602.2 23.1</b>
	<b>30</b>	<b>600.8 23.1</b>
	<b>31</b>	<b>600.8 23.1</b>
	<b>32</b>	<b>597.6 23.0</b>
	<b>33</b>	<b>591.6 22.7</b>
	<b>34</b>	<b>589.6 22.7</b>
	<b>35</b>	<b>577.2 22.2</b>
	<b>36</b>	<b>576.6 22.2</b>
	<b>37</b>	<b>576.2 22.1</b>
	<b>38</b>	<b>575.6 22.1</b>
	<b>39</b>	<b>573.8 22.1</b>
	<b>40</b>	<b>569.4 21.9</b>
	<b>41</b>	<b>566.2 21.8</b>
	<b>42</b>	<b>564.2 21.7</b>
	<b>43</b>	<b>563.2 21.6</b>
	<b>44</b>	<b>562.8 21.6</b>
	<b>45</b>	<b>562.6 21.6</b>
		<b>ALIGNMENTS</b>
		<b>RESULT 1</b>
		AK088868
		<b>LOCUS</b> AK088868
		<b>DEFINITION</b> Mus musculus 2 days neonate thymic cells cDNA, RIKEN
		full-length enriched library, clone:R430059G08 product:secreted
		frizzled-related sequence protein 1, full insert sequence.
		<b>ACCESSION</b> AK088868
		<b>VERSION</b> AK088868.1
		<b>KEYWORDS</b> HTC, CAP trapper.
		<b>SOURCE</b> Mus musculus (house mouse)
		<b>ORGANISM</b> Mus musculus
		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Eucarchontoglires; Glires; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
		<b>REFERENCE</b>
		<b>AUTHORS</b> Carninci, P. and Hayashizaki, Y.
		<b>TITLE</b> High-efficiency full-length cDNA cloning
		<b>JOURNAL</b> Meth. Enzymol. 303, 19-44 (1999)
		<b>PUBLMED</b> 10349636
		<b>REFERENCE</b>
		<b>AUTHORS</b> Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
		<b>TITLE</b> Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
		<b>JOURNAL</b> Genomic Res. 10 (10), 1617-1630 (2000)
		<b>PUBLMED</b> 11042159
		<b>REFERENCE</b>
		<b>AUTHORS</b> Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitzusai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, T., Towa, Y., Iwasa, M., Ohara, B., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inouye, Y., Kira, A., and Hayashizaki, Y.
		<b>TITLE</b> BQ932355
		<b>JOURNAL</b> Genomic Res. 10 (11), 1757-1771 (2000)
		<b>PUBLMED</b> 11076861
		<b>REFERENCE</b>
		<b>AUTHORS</b> The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
		<b>TITLE</b> Functional annotation of a full-length mouse cDNA collection
		<b>JOURNAL</b> Nature 409, 685-690 (2001)
		<b>PUBLMED</b> 5
		<b>REFERENCE</b>
		<b>AUTHORS</b> The FANTOM Consortium and the RIKEN Genome Exploration Research

## SUMMARIES

Maximum Match 10  
Listing first 40

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
```

```
2: /cgns_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgns_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgns_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
```

ee : Listing first 45 summaries  
Published Applications NA Main:\*

processing: Minimum Match 0% Maximum Match 100%

number of hits satisfying chosen parameters: 1958/084

ed: 9793542 seqs, 4134689005 residues

g table: IDENTITY NUC  
ace: 1 gatctggctggggactggcc.....gaagttagttttaaaaaaaad 200

US-10-666-851-1  
3200

May 7, 2006, 13:55:19 ; Search time 1855 Seconds  
(without alignments)

1020 *Journal of Health Politics, Policy and Law*

GenCore version 5.1.8

ALIMENTI

Sequence 1, Application US10666851  
Publication No. US20040115195A1  
GENERAL INFORMATION:  
APPLICANT: Bodine, Peter  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS USING SECRETED FRIZZLED  
TITLE OF INVENTION: PROTEIN  
FILE REFERENCE: 00630/100M091-US1  
CURRENT APPLICATION NUMBER: US10/666,851  
CURRENT FILING DATE: 2003-09-19  
PRIOR APPLICATION NUMBER: US 10/169, 545  
PRIOR FILING DATE: 2002-05-31  
PRIOR APPLICATION NUMBER: US 60/412, 379  
PRIOR FILING DATE: 2002-09-19  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 1  
LENGTH: 2602  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-666-851-1

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GenCore version 5.1.8

OM nucleic - nucleic search, using sw model  
 Run on: May 7, 2006, 09:55:34 ; Search time 2747 Seconds  
 (without alignments)  
 6312.898 Million cell updates/sec

Title: US-10-666-851-1

Perfect score: 2602

Sequence: 1 gatctgtggggactgcgcc.....gaagtagttctaaaaaaa 2602

Scoring table: IDENTITY\_NUC

GAPOP 10.0 , Gapext: 1.0

Searched: 4996997 Bseqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing First 45 summaries

Database :

N\_Geneseq\_21:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003c:\*

11: geneseqn2003db:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2602	100.0	2602	12 ADP68535
2	254.8	97.4	4451	8 ABZ02226
3	2534.8	97.4	4616	4 AAH72901
4	2533.2	97.4	4497	2 AAV43495
5	2517.2	96.7	4462	8 ABX77526
6	2465.4	94.8	4469	4 AAS12954
7	2465.4	94.8	4469	6 ABT0165
8	2465.4	94.8	4469	8 ABZ34845
9	2465.4	94.8	4469	12 ADP21417
10	2465.4	94.8	4469	13 ADP24996
11	2465.4	94.8	4469	13 ADP19015
12	2465.4	94.8	4469	13 AEG4538
13	2465.4	94.8	4469	14 ADV44809
14	2465.4	94.8	4469	14 ADX8915
15	2302.8	88.5	4245	4 AAF80506
16	2302.8	74.1	3670	2 AAZ33577
17	1871.4	71.9	3872	13 ADP07183
18	1844.6	70.9	2094	8 ABZ82228
19	1787.8	68.7	2075	6 ABV73022

#### ALIGNMENTS

20	1787.8	68.7	2075	6 ABV73022	Abv73022 Human sec
21	1787.8	68.7	2075	8 ABX75330	Abx75330 Human sec
22	1787.8	68.7	2075	8 AAD52558	Aad52558 PRP DNA
23	1787.8	68.7	2075	12 ADP43319	Adp43319 Human sec
24	1787.4	68.7	2075	10 ADC71197	Adc71197 Human sec
25	1781.6	68.3	2075	8 ABZ81830	Abz81830 Receptor
26	1483.4	57.0	3215	3 ARACT657	Aact657 Human can
27	1468.4	56.4	3216	2 AAZ23608	Aaz23608 Human bre
28	1452.8	55.8	3180	2 AAZ42127	Aaz42127 Human nor
29	1076.2	41.4	1308	2 ARV1915	Arv1915 Human sec
30	996.4	38.3	1247	13 ACNA1451	Acn1451 Human dia
31	925.8	35.6	942	9 ACC81035	Acc81035 Human sec
32	925.8	35.6	942	6 ABV73023	Abv73023 Human sec
33	912.6	35.1	942	10 ADC71198	Adc71198 ORF of th
34	912.6	35.1	942	12 ADH43320	Adh43320 Human sec
35	909.6	35.0	1017	10 ADC71192	Adc71192 DNA encod
36	909.6	35.0	1017	10 ADH43314	Adh43314 Human sfr
37	909.6	31.9	945	9 ACC81034	Acc81034 Murine em
38	899.8	31.9	945	9 ACC81034	Acc81034 DNA encod
39	697	26.8	804	10 ADC71195	Adc71195 Human sec
40	697	26.8	804	10 ADC71194	Adc71194 DNA encod
41	634	24.4	741	10 ADH43316	Adh43316 Human sec
42	634	24.4	741	12 ADH43316	Adh43316 Human sec
43	628.8	24.2	1146	8 ABX75340	Abx75340 Human cDN
44	628.8	24.2	1146	8 ADP52570	Adp52570 SRPP 1 DN
45	628.8	24.2	1146	8 ABZ81842	Abz81842 WIF-1 nuc

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 7, 2006, 13:22:06 ; Search time 12942 seconds  
 (Without alignments)  
 11428.424 Million cell updates/sec

Title: US-10-666-851-1

Perfect score: 2602

Sequence: 1 gatctgtggggactggcc.....gaagtagttctaaaaaaa 2602

Scoring table: IDENTITY NUC

Gappen 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : GenBank\*

1: gb\_ba:\*

2: gb\_ini:\*

3: gb\_env:\*

4: gb\_on:\*

5: gb\_ov:\*

6: gb\_pac:\*

7: gb\_pini:\*

8: gb\_prc:\*

9: gb\_ror:\*

10: gb\_rts:\*

11: gb\_sy:\*

12: gb\_uu:\*

13: gb\_vr:\*

14: gb\_hgt:\*

15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No. Score Query Match Length DB ID Description

### ALIGNMENTS

ORIGIN	SEQUENCE	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	COMMENT
AX099741 Sequence	AX099741	Sequence 1 from Patent WO0119855.	AX099741	2602 bp				
AR253209 Sequence	AR253209							
BC036503 Homo sapi	BC036503							
CS025753 Sequence	CS025753							
AX235102 Sequence	AX235102							
AX578081 Sequence	AX578081							
AR056887 Homo sapi	AR056887							
AR129158 Sequence	AR129158							
BD135588 Human nuc	BD135588							
AX017498 Sequence	AX017498							
CO850220 Sequence	CO850220							
AK127331 Homo sapi	AK127331							
AR017987 Homo sapi	AR017987							
AR253205 Sequence	AR253205							
AC103846 Homo sapi	AC103846							
AC104393 Homo sapi	AC104393							
AR253206 Sequence	AR253206							
AR361924 Sequence	AR361924							

Database : GenBank\*

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